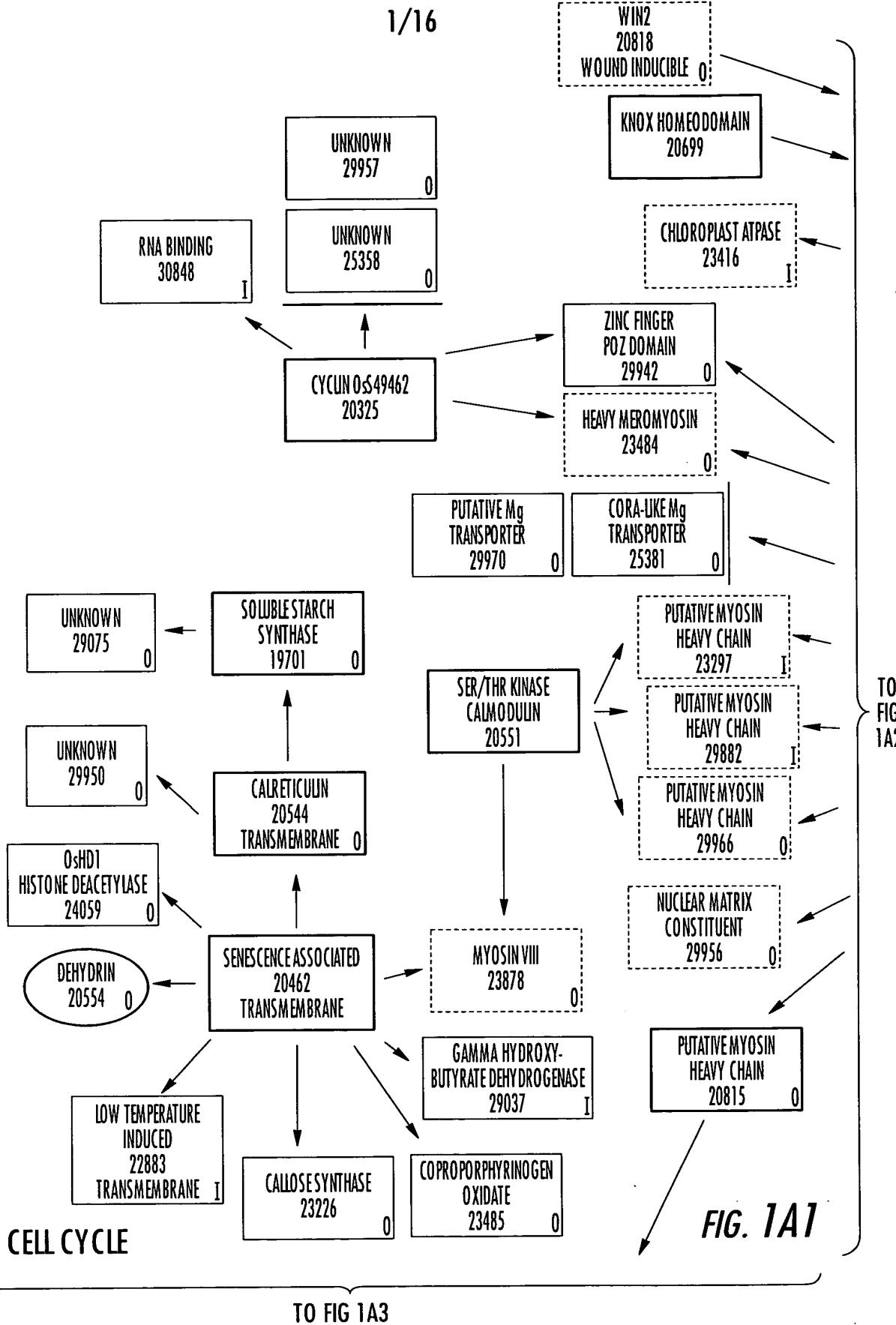


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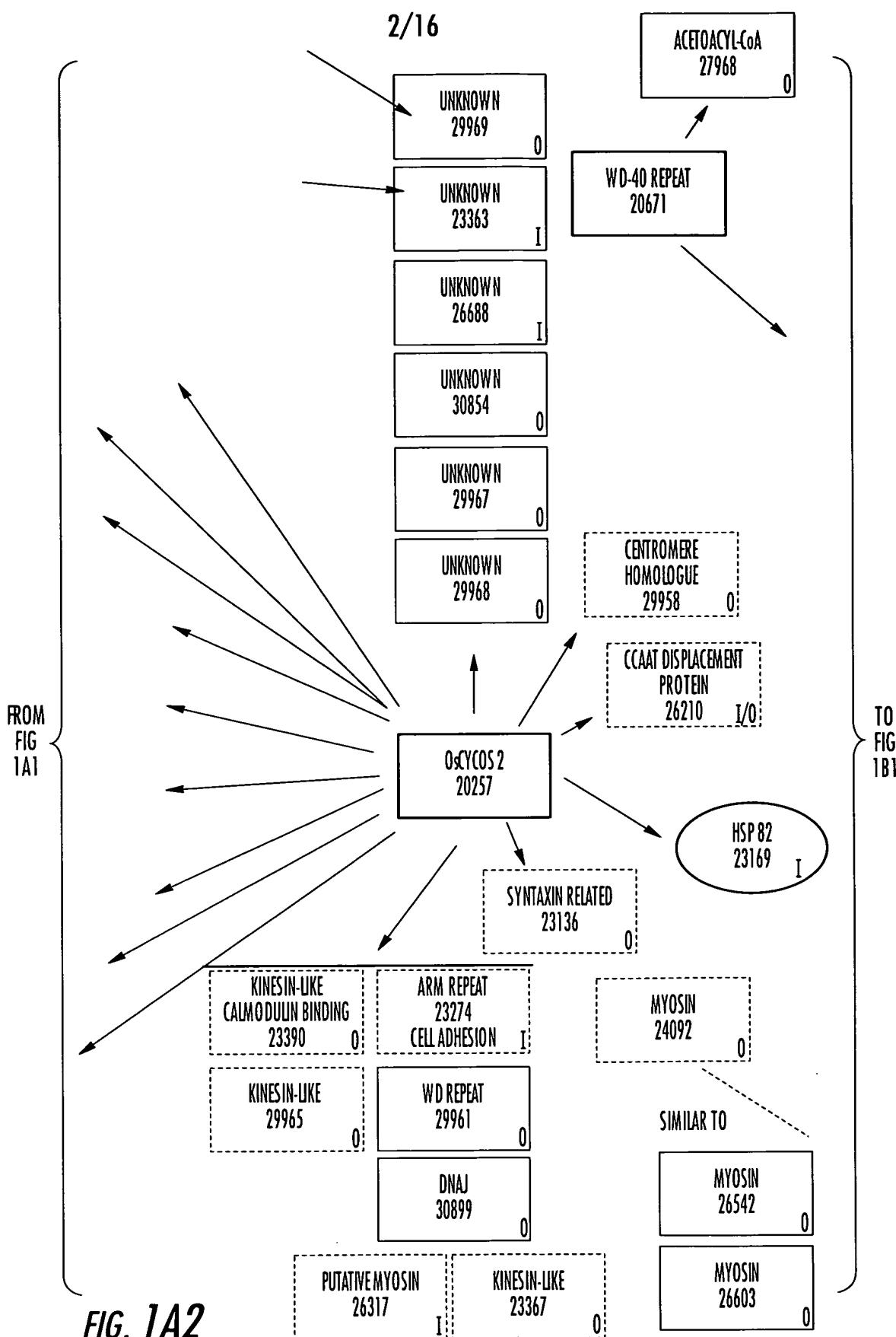


FIG. 1A2

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FROM FIG 1A2

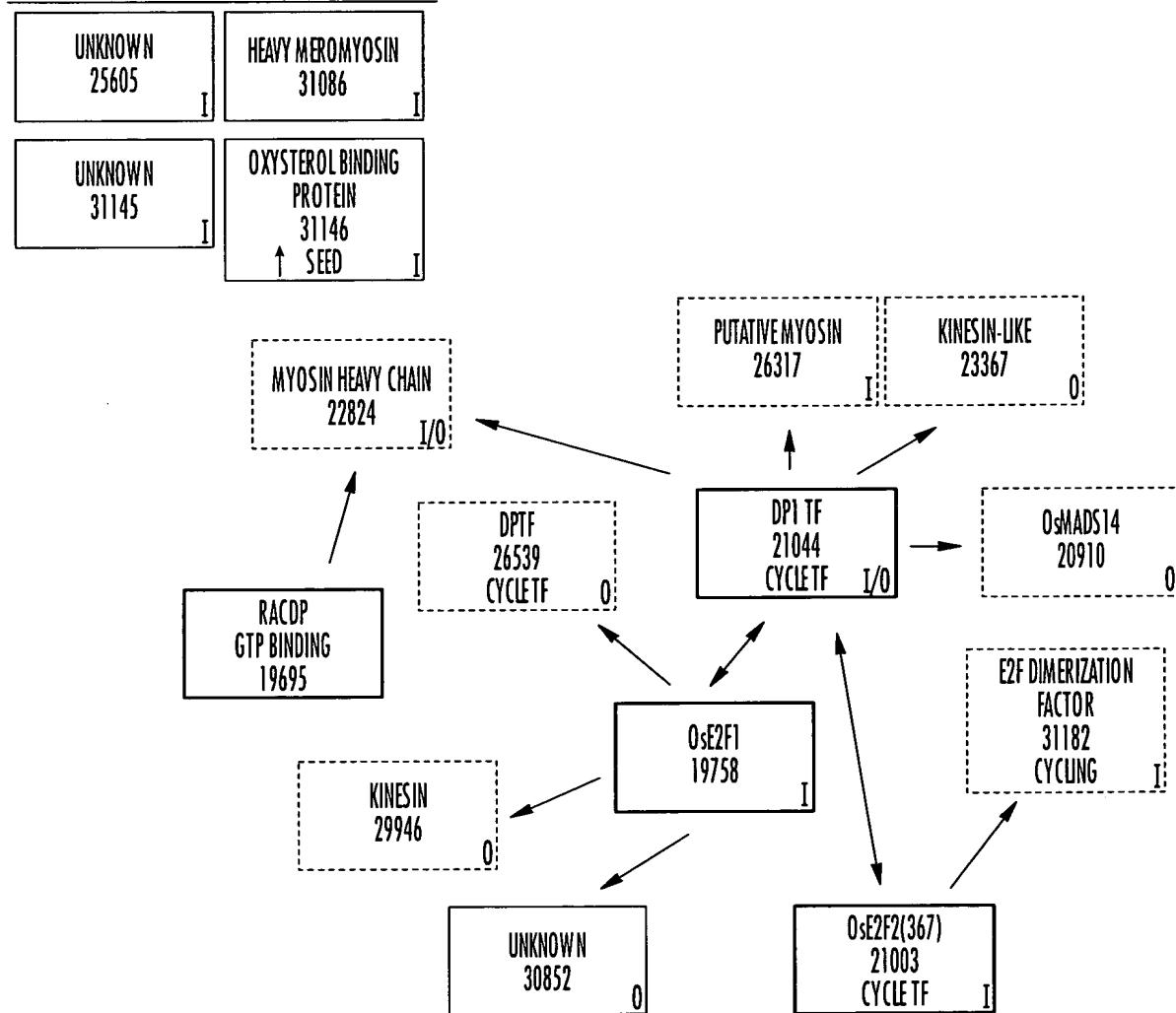
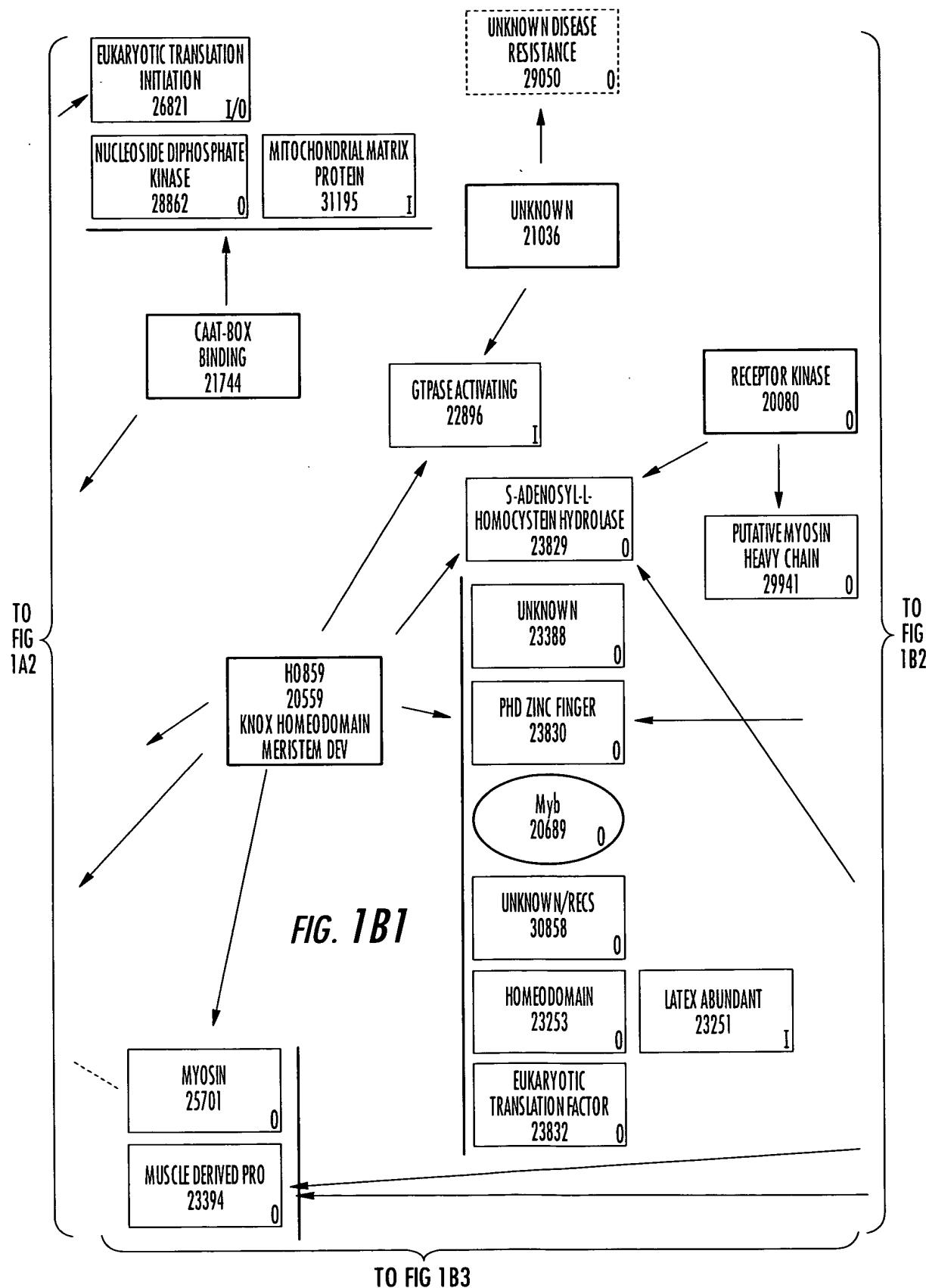


FIG. 1A3

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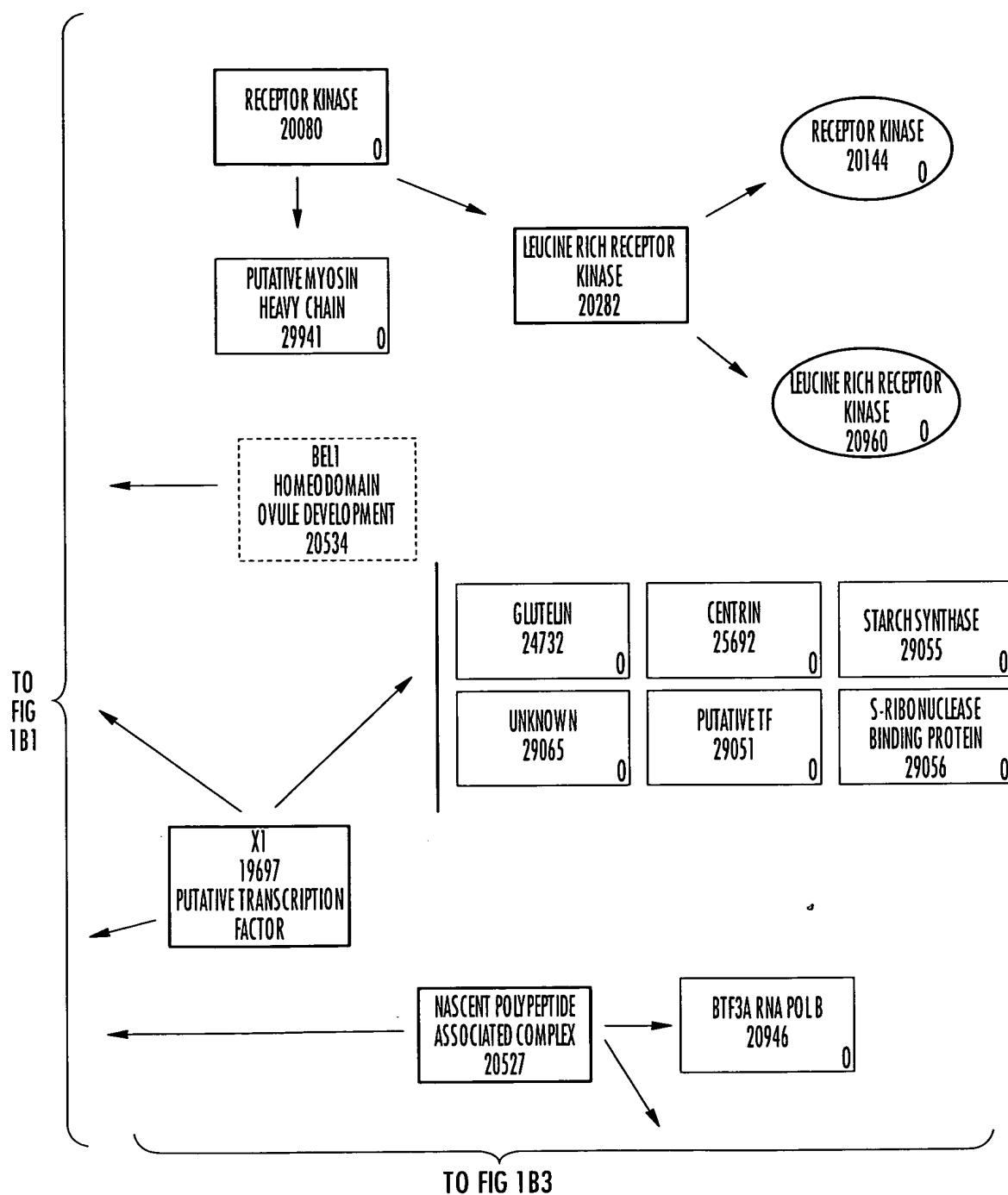


FIG. 1B2

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TO FIG 1B1 AND 1B2

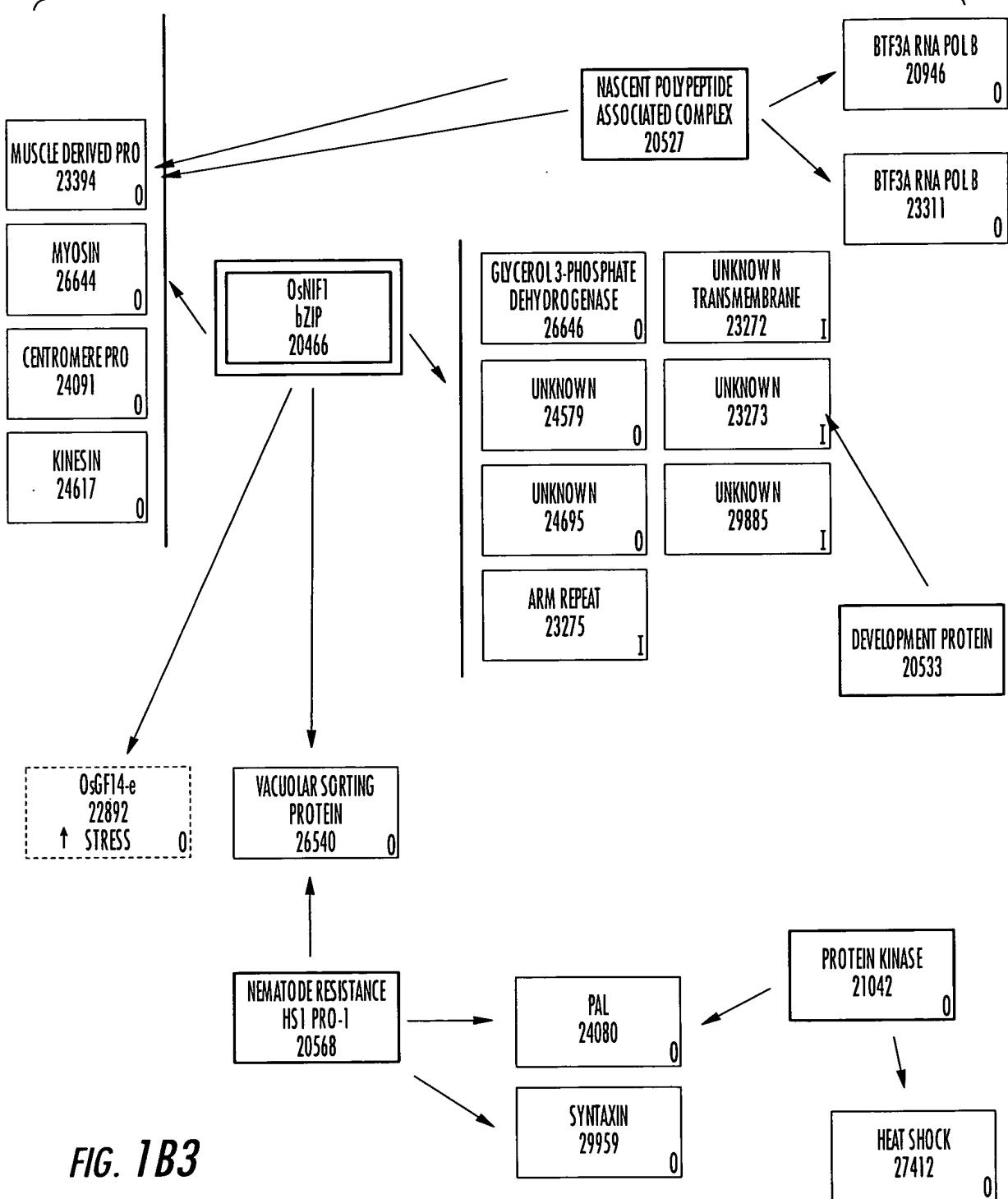
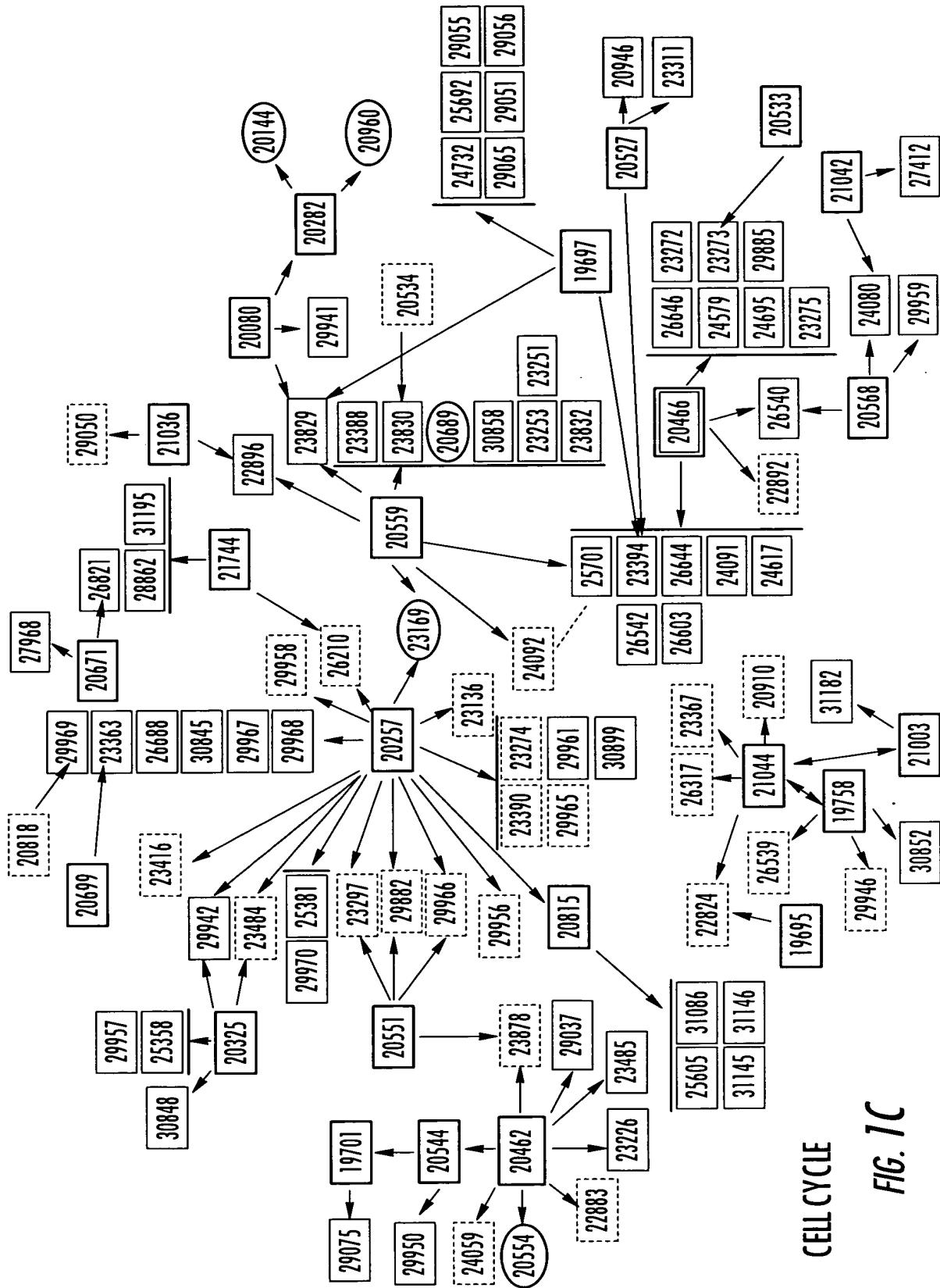


FIG. 1B3

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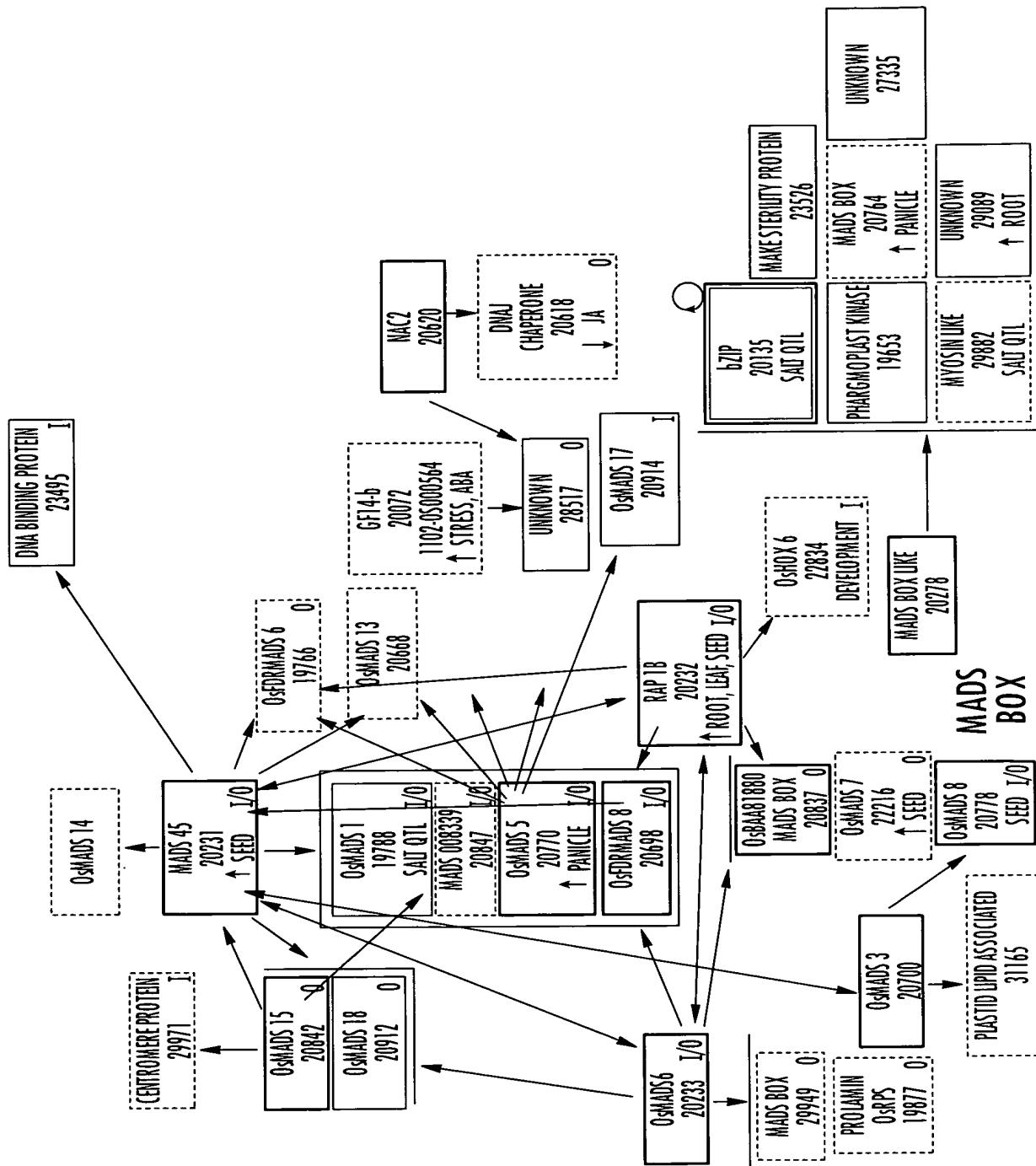
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FIG. 2



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CONS.	-----MGRGRVELKRIENKINRQVTGSKRRNGLLKKAYELSVLCDAEVALIITSSRGKLYEFASSS	10	20	30	40	50	60	70
19766	-----MGRGKVKLRIENTINRQVTFSKRRSGLLKKANEISVLCDAEVALIITSTKGKLYKYYATDS							
19788	-----MGRGKVELKRIENKISRQVTFAKRRNGLLKKAYELSLLCDAEVALIITSGRGRGLFEEFSSSS							
20231	-----MGRGRVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIITSNRGKLYEFCSTQ							
20232	-----MGRGKVKLRIENKINRQVTFSKRRSGLLKKANEISVLCDAEVALIITSTKGKLYEYATDS							
20233	-----MGRGRVELKRIENKINRQVTFSKRRNGLLKKAYELSVLCDAEVALIITSSRGKLYEFGSAG							
20278	-----MGRGKIEIKRIENATNRQVTYSKRRTGIMKKARELTVLCDAQVAITMFSSTGKYHEFCSPS							
20668	-----MGRGRRIEIKRIENTTSRQVTCKRRNGLLKKAYELSVLCDAEVALIVFSSRGRLYEEYNNNN							
20698	MV-----RGRTELKRIENPTSRQVTFSKRRNGLLKKAFELSVLCDAEVALIVFSPRGRLYEFASAP							
20700	-----MGRGKIEIKRIENTTNRQVTFCRKRRNGLLKKAYELSVLCDAEVALIVFSSRGRLYEEYANNS							
20770	-----MGRGKVELKRIENKISRQVTFAKRRNGLLKKAYELSVLCDAEVALIITSTRGRLFEEFSTSS							
20778	-----MGRGRVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIITSNRGKLYEFCSGQ							
20837	MA-----RERREIKRIESAAARQVTFSKRRRGFLKKAAEELSVLCDADVALIVFSSSTGKLSHFAS-S							
20842	-----MGRGKVKLRIENKINRQVTFSKRRNGLLKKAAHEISVLCDAEVAIAIVFSPKGKLYEYATDS							
20847	ESEG--RAATGKRERIAIRRIDNAAARQVTFSKRRRGFLKKAAEELSILCDAEVGLVVFATGKLHQFAS-T							
20910	-----MGRGKVKLRIENKINRQVTFSKRRSKLLKKANEISVLCDAEVALIITSTKGKLYEYATDS							
20912	-----MGRGPVQLRRIENKINRQVTFSKRRNGLLKKAAHEISVLCDADVALIVFSTKGKLYEFSSSH							
20914	-----MGRGRVELKRIENKINRQVTFSKRRNGLLKKAYELSVLCDAEVALIITSSRGKLYEFGSAG							
21116	LVGGSWRISIGMGRGRVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIITSNRGKLYEFCSTQ							
29949	-----MGRGKIVIRR1DNSTSROVTFSKRRNGLLKKAKELSILCDAEVGLVVFSSSTGXLYEFSSST-							

FIG. 3A

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CONS.	S-MTKTLLERYQRYSYA--ESAVISAESDTQGSWYQEYKLKAKVEALQQTQRH-----LLGEDLESLSLKELQ	80	90	100	110	120	130	140
19766	C-MDKILLERYSYAEK--VLISAESDTQGNWCHERYRKLAKVETIQKCQKH-----LMGEDLESLNLKELQ							
19788	C-MYKTLERYRSCNIN--SODAAAPENEI--NYQEYKLKTRVEFLQTQRN-----ILGEDLGPLSMEKE							
20231	S-MTKTLEKYQKCSYAGPETAVQNRESEQLKASRNELYKLKARVENLQRTQRN-----LLGEDLDSLGIKELE							
20232	C-MDKILLERYSYA--EKVLISAESDTQGNWCHERYRKLAKVETIQKCQKH-----LMGEDLESLNLKELQ							
20233	G-ITKTLERYQHCCYNAQDSNNALS--ET-QSWYHEMMSKLKAKFEALQRTQRH-----LLGEDLGPLSVKELQ							
20278	DIKGIFDRYQ-----QAIGTSLWIEQYENMORTLSHLKDINRNLRTETIRQRMGEDLDGLEFDEL							
20668	N-VKATIDRYKKHAHACGSTSGAPLIEVNAAQYYQOESAKLRLHQIOMLONTNKH-----LVGDNVSNLSLKELK							
20698	S-LQKTIIDRYKAYTKDHVNNTKTIQDIIQVK--DTTLGLAKKLEALDESRRK-----ILGENLEGCSIEELR							
20700	--VKSTTVERYKKANS-DTSNSGTVAEVNAQHY-QQESSKLRQOISSLQNANSR-----TIVGDSINTMSLRLDK							
20770	C-MYKTLERYRSCNINLNNSCEASAALETEL-SNYQEYKLKTRVEFLQTQRN-----LLGEDLVLPLSLKEL							
20778	S-MTRTLERYQKFSYGGPDATIONKENELVQSSRNELYKLKARVENLQRTQRN-----LLGEDLGLTGLGIKELE							
20837	S-MNEIIIDKYNTHSNNLGKAEPQLDNLNEHS--K-YAHLNEQLAESLRLRQ-----MRGEELEGLSIDELO							
20842	R-MDKILLERYSYA--EKALISAESSESEGNWCHERYRKLAKVETIQKCQKH-----LMGEDHESLNLKELQ							
20847	S-MEQIIIDRYNHSKTLQRAEPSOLDLQGEDS--STCARLKEELAETSLRLRQ-----MRGEELHRLNVEQLQ							
20910	C-MDKILLERYSYA--EKVLISAESDTQGNWCHERYRKLAKVETIQKCQKH-----LMGEDLESLNLKELQ							
20912	S-MEGILLERYQYSFD--ERAVLEPNTEDQENWGDEYGLKSKLDALQKSQRQ-----LLGEQLDLTLTKELQ							
20914	G-INKTLERYKNSCCYNAQGSNSALAGGEH-QSWYQEMSRLKTKLECLQRSSQRH-----MLGEDLGPLSIKELO							
21116	S-MTKTLEKYQKCSYAGPETAVQNRESEQLKASRNELYKLKARVENLQRTQRN-----LLGPDLDLDSLGIKELE							
29949	N-MKTVIDRYTNAAKEELLGGNAT--SEIKIWQREAAASLRQQLH-NLQESHKQ-----LMGEELSGLGVRDLQ							

FIG. 3B

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CONS.	QLEQLESSLIKHIRSRKTQLLIEQISELQRKEKSQLEENKVVLQKLVETEK--GQQVQQQG-WDQGGQGQTP	150	160	170	180	190	200	210
19766	QLEQQLENSLIKHIRSRKSQQLMLESINELQRKEKSQLEENKVVLQKELVEKQK---VQKQQQ-VQWDQTQPQT-							
19788	QLENQIEVSLKQIERSRKNQALLDQLFDLKSKEQQQLDNLKDRKKLQETS----AENVLHMSWQDGHHSGS							
20231	SIEKQOLDSSLIKHVRTRTRTKHLVDQLTTELQRKEQMVSSEANRCLRRKLEESNHVR-GQQVWEQGCNLLIGYERQP							
20232	QLEQQLENSLIKHIRSRKSQQLMLESINELQRKEKSQLEENKVVLQKELVEKQK---VQKQQLQ-WDQTQPQT-							
20233	QLEKQLECALSQARQRKTQLMMEQVEELRRKERQLGEINRQLKHKLEVEGSTS-NYRAMQQASWAQQGAVVEN							
20278	GLEQNVDAALEALKEVRRHKYHVITQTETYKKVKHSYEAYETLQQELGLREEPAGFVUDNTGGWDGGAGAGA							
20668	QLESRLEKGIAKTRARKNELLASEINYMAMKREIELQNDNMIDLRTKIAEEQQL-QQVTVARSAAMELQAAA							
20698	GLEMKLEKSLHNIRLKKTELLERQIAKLKEKERTL-----LKDNEENLR-GKHRNLLJAAALVANHMTT							
20700	QVENRLEKGIAKIRARKNELLAYAEVTEYMQKREVELQNDNMYLRSKVVENERGQ-QPLNM-----MGAASTSE							
20770	QLENQIEISLMNIRSSKNNQQLLDQVFELKREQQDANKDLKRKIQETS---GENMLHISCDVGPSSG--							
20778	QLEKQOLDSSLRHIRSTRTRQHMLDQLTDLQRREQMLCEANKCLRRKLEESNQLH-GQ-VWEHGATLLGYERQS							
20837	QLEKNLEAGLHRVMLTKDQQFMEQIISELQRKSSQLAENNMLRNQV-----SQ							
20842	QLEQQLESSLIKHIIISRKSHMLLESISELQKKERSLQEEENKALQKELVERQKNV-RGQQQVQG-WDQTQVQAO							
20847	ELEKSLESGLGSVLTKSKKILDEIDGLERKRMQLIEENRLKEQV-----SR							
20910	QLEQQLENSLIKHIRSRKSQQLMLESINELQRKEKSQLEENKVVLQKELVEKQK---VQKQQVQ-WDQTQPQT-							
20912	QLEHQLEYSLKHIRSKKKNQLLFESISELQKKKEKSILKNQNNVNLQK-LMETEKEK-NNAIINTN-REEQNGATP							
20914	QLEKQLEYSLSQARQRKTQIMMEQVDDRRKERQLGELNKQLNKLEADSS-NCRSAIQDSWVHGTVVSG							
21116	SIEKQOLDSSLIKHVRTRTRTKHLVDQLTTELQRKEQMVSSEANRCLRRKLEESNHVR-GQQVWEQGCNLLIGYERQP							
29949	GLENRLEISLRNIRMRKDNLKSEIEELHVKGSLIHQENIELSRSLNVMSQOK--LELYNKQACEQATDAN							

FIG. 3C

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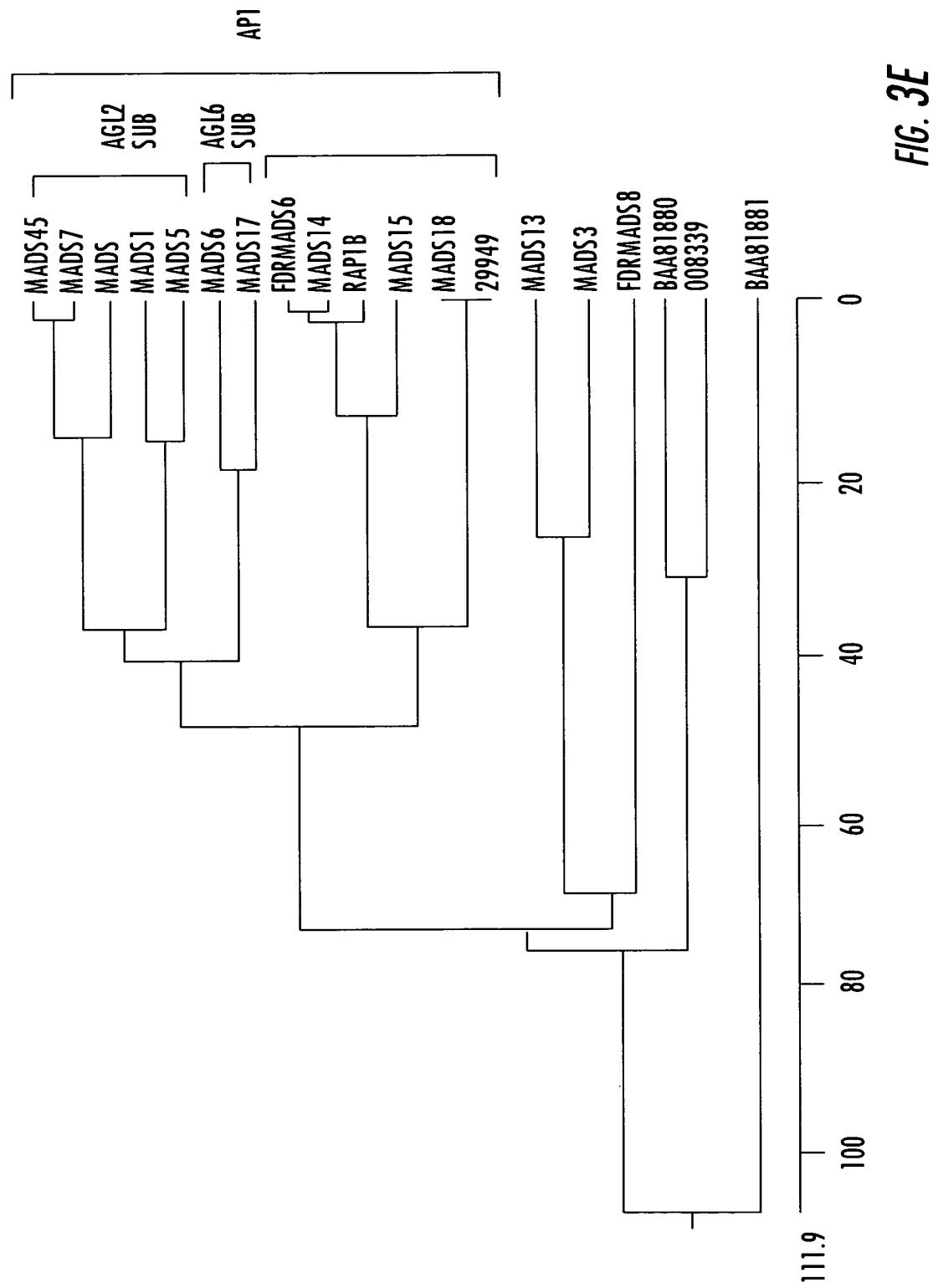
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CONS.	--A--QQ--PPHSSS--F--HREAA--EPTLNIGY---AAGERIA-----Q-----LPP--WML-----
220	230
240	250
260	270
280	290
19766	-----SSSSSFMMREA---LPTTNISNYPAAAGERIEDVAAGQPO-----HVRIG-LPP--WMLSHING
19788	STVLADQP--HHHQGLLHPHPDQGDHSLQIGYHHPHAHHHQAYMDHLSNEAADMVAAHPNEHIPS GWI-----
20231	--EVQQ--PLHGGNGFFFHPLDAAGEPTLQIGY---PAEHHEA-----MNSACMNTYMP--WLP-----
20232	-----ISSSSSFMMREA---LPTTNISNYPAAAGERIEDVPAGQPO-----HVRIG-LPP--WMLSHING
20233	GAAYVOPPPHSA-----AMDSEPTLQIGYPHOFVPAEAN-----TIGRSTA PAGAENNF M-LGWV L-----
20278	AADMFAFRVVPVSQPNLHGMAYGGNHD LRL-----G
20668	AQQQQNPFVAAAAQLDMKCFFPLNLFEAAAQVQAVA AQRQQI I PTELNLGYHHHLAIPGATAADAPP HF-----G
20698	TTAPAAWPRDVPMTSSTAGAADAMDVETDLYIGLPCTERSN RSET-----G
20700	YDHMVNNP Y-----DSRNFLQVNIMQQPOHYA-----HQLQPTTLQLG-----QQPAFN-----
20770	-----NAS-EANQEFLHH--AICDPSLHIGY-----QAYMDHILNQ-----
20778	PHAVQQVPPPHGGNGFFFHSLLEAAEPTLQIGF---TPEQ-----MNNSCVTAFMPT-WLP-----
20837	ISPEA--KQVVDTENFVTEGQESVMTALHGS S S Q S Q D N D G S D V S L K LG-----LPCGAWK-----
20842	AQAPOQAQTSSSSSSMLRDOOALLPPONICYPVMMGERNDAAA AAVA A Q GOVQLRIGGLPP--WMLSHLNA
20847	MSRMEEMQGPGDSEIVYEEQESVTNASYP--RPPPDMDSSDTSLKLG-----LHS-----
20910	-----SSSSSFMMREA---LPTTNISNYPAAAGERIEDVAAGQPO-----HERIG-LPP--WMLSHING
20912	STS SPTPVTADP-----IPTTNNSQSOPRGSGESEAQPSA QAGNSK-----LPP--WMLRTSH T
20914	GRVLNAQPP--P-----DIDCEPTLQIGY-YQFVRPEA-----NPRSNGGGDQNNNNF V-MGWPL-----
21116	--EVQQ--PLHGGNGFFFHPLDAAGEPTLQIGY---PAEHHEA-----MNSACMNTYMPWLP-----
29949	--ESSSTPYSPSFRIONANMPPSLELS-QSQQ--REGECSKTA-----APELGL-----HLP

FIG. 3D

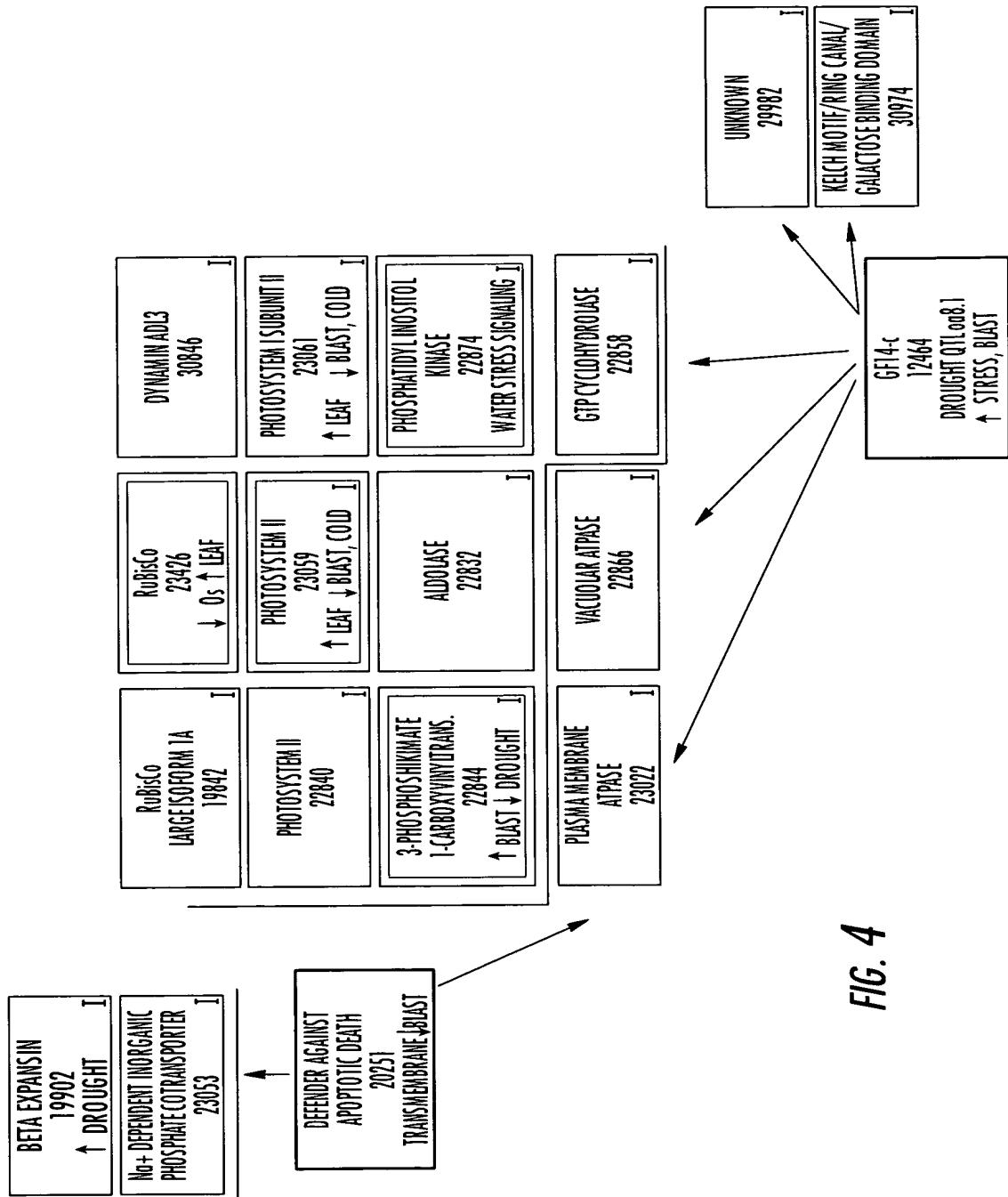
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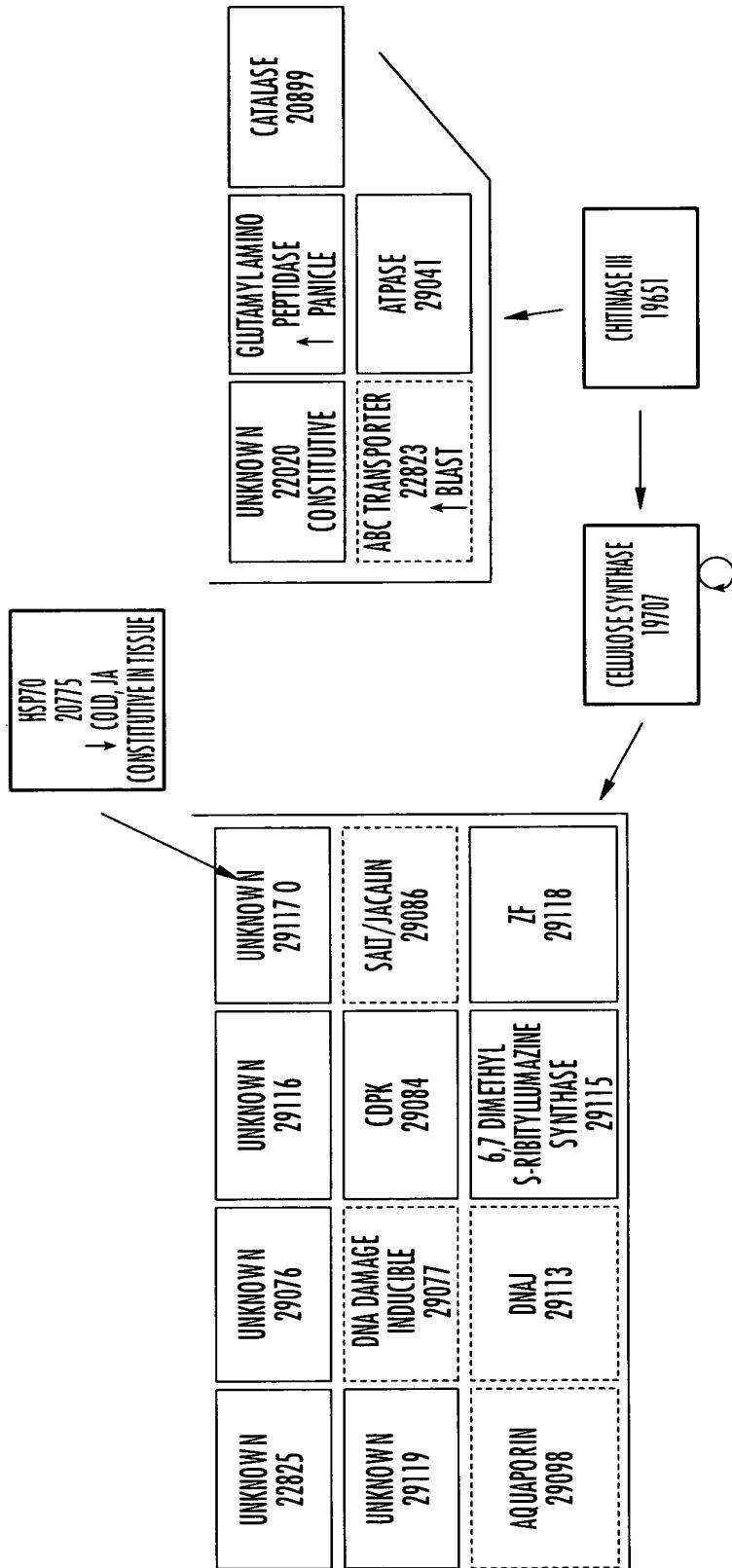


FIG. 5

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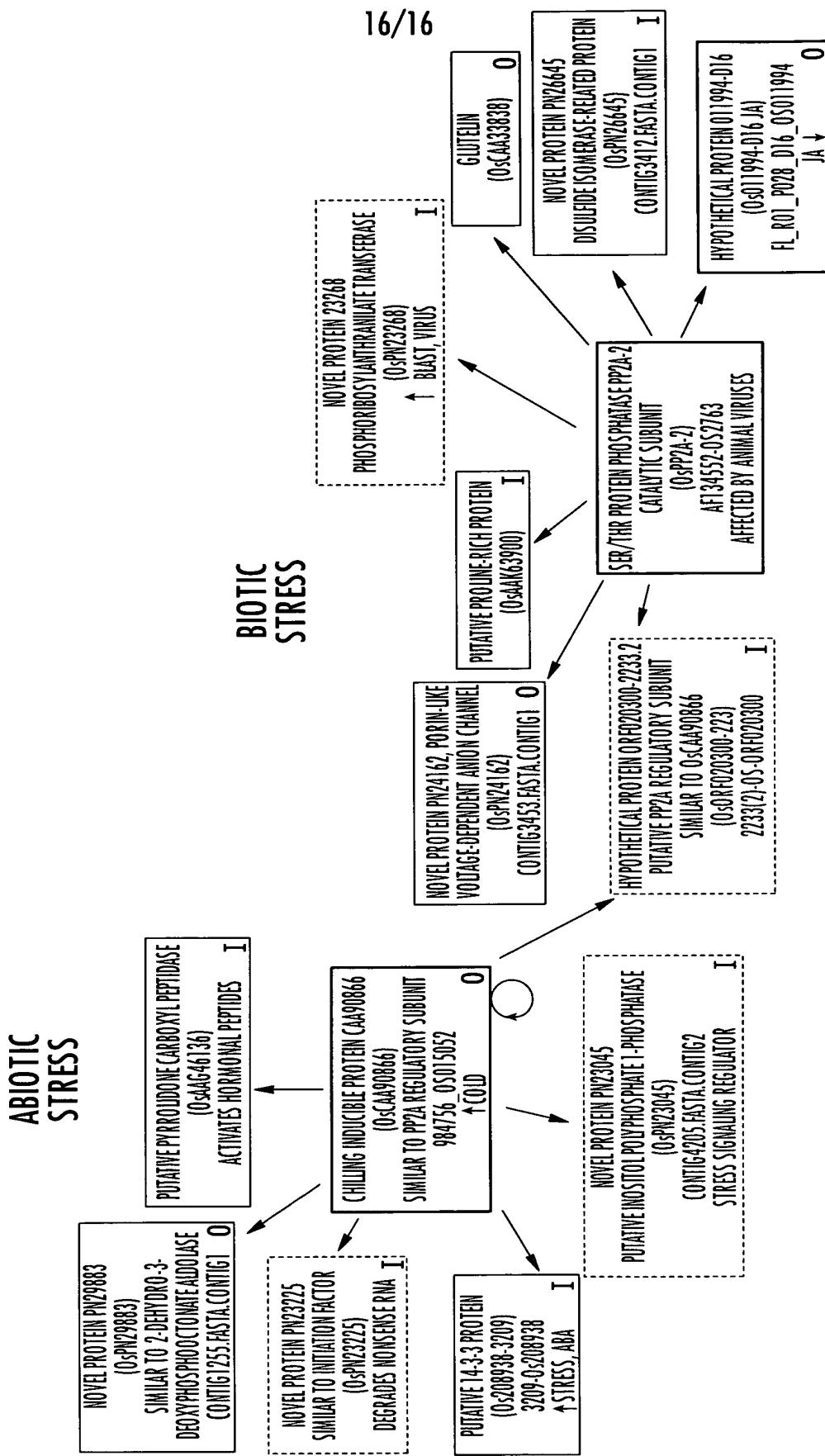


FIG. 6